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12 Wheat rust disease identification using deep learning

Abstract: Automated image-based tools are required when a human assessment of plant disease identification is expensive, inappropriate, or unreliable. Thus, there is a need to recognize cost-effective automated computational systems and image-based tools for disease detection that would facilitate advancements in agriculture. Deep learning (DL) is the deep neural network that uses multiple levels of abstraction for hierarchical representation of the data. Convolutional neural network model is used, in this chapter, on 2,000 images to identify the wheat rust disease in an unseen leaf image. The results show that DL has the potential to identify plant diseases with much higher accuracy.

Keywords: plant disease, wheat rust, CNN, deep learning, artificial intelligence

12.1 Introduction

The emerging challenge to the food security due to the decrease in annual crop production has become a topic of concern for the governments worldwide. Many known biotic and abiotic factors play a significant role in the crop loss, of which the plant diseases are the considerable ones. Traditionally, crop inspection and plant disorders identification were performed by farmers or experts with their naked eye. This requires detailed knowledge of disease symptoms and the experience of actual disease identification. Even with experience, this manual method is not feasible for larger fields as it requires continuous monitoring. Due to the variation and complexity of similar disease symptoms, even the agronomists or plant pathologists fail to detect specific crop diseases accurately with naked eyes. Automated image-based tools are required for the identification of complexity in plant diseases because human assessment can sometimes be inappropriate and unreliable [1, 2]. There is a need for developing cost-effective automated computational systems and image-based tools for disease detection that would facilitate advancements in agriculture [3]. In this new era of computation, in recent years, implication of artificial intelligence (AI) has been growing fearlessly and

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contributes to the development of innovative methodologies and models among which deep learning (DL) is the most prominent one [4]. With DL, computational models use the different levels of abstraction for the hierarchical representation of data. This chapter emphasizes the potential of DL to identify plant diseases with much higher accuracy.

The four phases involved in plant disease identification are namely image acquisition, image preprocessing, features extraction, and classification [5]. In image acquisition, the acquired images are converted into the preferred output format for further processing. Images may be self-acquired by authors or maybe any benchmarking dataset such as the PlantVillage database [6]. The procedure of image preprocessing aims at highlighting the region of interest (disease infected area) in plant leaves [7]. Image preprocessing commonly involves image segmentation [8–11], image enhancement, and color space conversion. The image of a leaf is filtered from unnecessary background, and RGB colors are converted into color space parameters [12, 13]. Furthermore, that image is segmented to a meaningful part, which is much easier to analyze. Unfortunately, removal of background is quite difficult and in some scenarios, automation of the system performs poorly due to user intervention [13]. In the case of feature extraction, feature vectors are constructed from the features extracted from the images manually. This type of extraction could be statistical or structural, for example, in the use of color moments in the extraction of color statistics [14], the extraction of all multiscale features is being done by combining Gabor transform and wavelet transform [15]. Many previous studies have also reported the use of gray-level co-occurrence matrix [14–18] to extract texture features. However, advantage of DL is the automatic feature extraction, which ultimately holds a good contribution in higher accuracy when compared with other conventional techniques discussed [19–25].

The last phase of plant disease identification is a classification where the classification model is implemented to identify the existing plant disease in the images. The model used for the identification must be well trained with learning algorithms and must have already seen disease images. Techniques for disease identification can be mainly classified into two types: image processing-based techniques and machine learning techniques. For disease identification, image processing techniques are necessarily followed by some machine learning methods that can perform on large datasets. On the other hand, machine learning methods can work on image-based datasets as well as textual attribute-based data that do not require an image. For disease identification using attribute-based tables, one need not use image processing techniques, but other data cleaning and preprocessing should be followed. In machine learning, algorithms are capable of learning on their own from input data according to the objective. In machine learning, high performance along with statistical pattern recognition creates new opportunities in the agriculture domain with their improved sensitivity toward plant disease detection. The k -nearest neighbors [15, 26], support vector machine [12, 16, 27], and artificial neural network (ANN) [28–30] represent the

commonly used learning algorithms as per the literature. On the other hand, neural networks, which understand complex data, have found its applications in extraction and detection of patterns that are quite difficult to be observed by the human brain or other computer techniques. Moreover, the features like adaptive learning, real-time operations, and self-organization increase the acceptability for ANNs. ANN is a well-organized model comprising different layers connected to its consecutive layer. In this chapter, authors emphasize on the application of DL, particularly on the convolutional neural network (CNN), for developing a model for plant disease identification.

12.2 Deep learning and crop disease identification

In plant pathology, the implementation of DL in leaf image classification and plant disease identification has started to gain momentum in recent years. In this approach, during the training phase, feature extraction from the data is done automatically. To verify the superiority of DL models over state-of-the-art methods, we have reviewed both small and large dataset studies containing 500–87, 848 images [31–33]. A literature review on DL shows its better accuracy and efficiency over other techniques [19]. The conventional machine learning techniques and image processing techniques are only successful under limited and constrained systems. A comparison study on the CNN models and conventional pattern recognition techniques in plant identification using three different databases concluded that CNNs outperform the conventional methods [34].

Nigam et al. [35] reviewed the different implementation of DL in agriculture domain for identification of plant diseases and developed a CNN model to perform plant disease identification using wheat crop images of healthy leaves and yellow rust infected leaves through DL. The use of DL includes improvements in performance and high computational accuracy. Some factors affecting the CNNs performance in identification of plant diseases are limited annotated datasets, symptom representation, covariate shifts, image background, symptom segmentations, image capture conditions, multiple simultaneous disorders, symptom variations, and disorders with similar symptoms [36, 37]. In real-life conditions, the systems developed through DL have high performance and precision in detecting specific plant diseases. It can even be operated through a user-friendly mobile application for the detection of multiple diseases in plants [37, 38]. DL techniques can achieve accuracy between 90% and 99%.

DL is the deep neural network that learns the hierarchical data representations with the number of abstraction levels [39, 40]. The application of DL in plant pathology and specifically on leaf image classification and plant disease identification has started gaining momentum in recent years. One of the most powerful and basic DL tools for modeling complex processes such as image-based disease identification is CNNs.

12.3 Convolutional neural networks

In the case of image classification, CNN is more efficient than other DL models because of a smaller number of parameters involved and automatic feature extraction without any human supervision. A CNN mainly consists of three layers: convolution layer, pooling layer, and fully connected layers [19]. A CNN model has two components: feature extraction and classification (Figure 12.1). The convolution layer and pooling layers perform the feature extraction from the input images, whereas fully connected layers have their role in classification of the images into predefined classes.

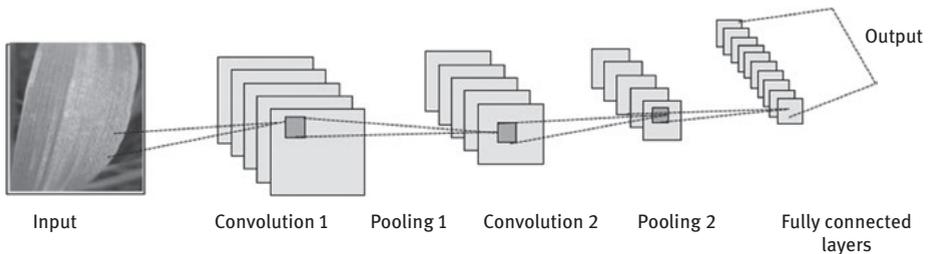


Figure 12.1: Convolution neural network architecture.

The different layers involved in CNN are explained as follows:

1. *Convolution layer:* This layer extracts features automatically from each input image. It basically consists of a set of learnable filters and learns the relationship between features using kernel or filters to produce a feature map. Each learnable filter is applied to the raw pixel values of the image in a sliding window manner, and computes the dot product between the filtered and input pixel. This results in a two-dimensional activation map known as a feature map. In simple terms, the network learns filters (i.e., edges and curves) that activate when there are known features in the input image. The values of these filters are learnt by the CNN during the process of training. Rectified linear unit is a activation function with output $f(x) = \max(0, x)$ that is used to introduce the nonlinearity in the CNN model.
2. *Pooling layer:* This layer reduces the size of convolution maps by downsampling, which decreases the training time and combats overfitting by retaining only the valuable information to process further. Max pooling is a commonly used pooling type, which takes the max value in the pooling window, whereas a mean value is taken in case of average and sum pooling. The output is given in the form of the maximum activation value and hence reduces the dimensionality of the feature.
3. *Fully connected layer:* Final pooling layer output (three-dimensional matrix) is flattened into a one-dimensional vector and that becomes the input to the fully

connected layer. These features are then combined to create a model. In the end, SoftMax or sigmoid activation function computes the predefined class scores and classifies the image into a predefined class.

12.4 Parameters and hyperparameters in CNN model

DL comprises parameters and hyperparameters. Parameters are the configuration variables whose value can be estimated or learned from the data, whereas variables of hyperparameters determine the network structure of a model. These are decided before the training of the network. Hyperparameters related to a network structure are as follows:

- *Batch and batch size:* It is the total amount of training examples present in a single set. Batch size is the number of subsamples given to the network for parameter updates. The optimum size is determined based on experiments as shown in Figure 12.1.
- *Epochs:* It refers to the times the training data is given to the network while training the model. Even though the training accuracy increases on increasing epochs, at some point, the validation accuracy starts decreasing. At that point, more epochs will lead to overfitting of model.
- *Hidden layers and units:* Middle layers are present between the input and the output layer. Layers can be added until the test error improves.
- *Activation function:* It introduces the nonlinearity in a model, which allows the learning of nonlinear prediction boundaries. SoftMax is used more often in the output layer while making multiclass predictions.
- *Learning rate:* It is defined as the speed of a network in updating its parameters while learning in a model. Usually, a decaying learning rate is mostly preferred.
- *Momentum:* It gives information about the direction of next step with the help of prior knowledge about previous steps and prevents oscillations. A momentum of 0.5–0.9 is generally chosen while training a model.

12.5 Software and hardware requirement

With an increasing focus on DL studies, many software prevail in the industry for automatic disease identification. Caffe, Tensorflow, and frameworks are used along with popular Python libraries such as Keras. MATLAB is used for the efficient pre-processing of images. Most recently, DL libraries are introduced in R software too. Caffe, Keras, Tensorflow, Theano, and Deeplearning4j are popular software that can be used for disease identification using CNN architecture models. Usually, the

hardware requirement is quite a challenge in DL. It needs high computational machines for faster training of the model. DL algorithms are mostly seen being implemented on the NVIDIA® graphical processing units in the Linux environment.

12.6 Case study of wheat rust

In this case study, 2,000 images containing leaves of the wheat plant were collected to develop AI-based model for wheat disease classification, and sample images are shown in Figures 12.2 and 12.3.



Figure 12.2: Healthy leaves.

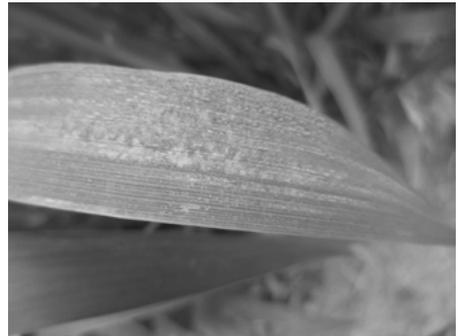


Figure 12.3: Rust infected leaves.

The author created a dataset of 2,000 images that consist of healthy leaves (1,000 images) and yellow rust infected leaves (1,000 images) (Table 12.1). Hardware specifications used for the experiment are presented in Table 12.2.

These images were captured keeping in mind the different sizes, orientations, and backgrounds. In the case study, Keras and Tensorflow are used as open-source libraries for DL. The graphical processing units facilitate the execution of DL algorithms faster as compared with central processing units. Furthermore, PyCharm is used as the python-integrated development environment for the programming interface. The main objective was to evaluate the model performance for unseen images of yellow rust infected leaves.

Table 12.1: Description of the dataset used.

Image dataset	Wheat yellow rust
Location	ICAR – Indian Agricultural Research Institute, New Delhi
Time period	January to April 2019
Devices used	Canon digital camera, OnePlus 6T phone
Images	2,000
Classes	Two

Table 12.2: Basic hardware specifications.

Hardware and software	Specifications
Operating system	Ubuntu
Processor	Intel Core i7-3930 CPU @ 3.60 GHz
Memory	32 GB
Graphics	NVIDIA GeForce GT 360
Environment	Anaconda with Keras
IDE	PyCharm

These hyperparameters are empirically determined as per the multiple experiments conducted on the author’s own image dataset according to the best results obtained for wheat disease identification. Hyperparameters related to CNN in our experiment are presented in Table 12.3.

Table 12.3: Hyperparameters used for the experiment.

Optimization algorithm	RMSProp
Base learning rate	0.01
Weight decay	0.001
Batch size	10
Loss function	BinaryCrossentropy
Activation function	Sigmoid
Epochs	60

As shown in Table 12.3, root mean square propagation (RMSprop) optimizer was used as it learns the appropriate set of weights and biases of the network and minimizes the loss function. Optimizers minimize the cost function by finding the optimized value for weights. In RMSprop, the learning rates get adjusted automatically, and it chooses a different learning rate for each parameter. Besides, other optimizers can be used such as Adam, Adadelata, and stochastic gradient descent (SGD). The base learning rate is a configurable hyperparameter that controls the rate at which the network learns. For example, learning rate of 0.01 means weights in the network are updated ($0.01 \times$ estimated error) each time. Weight decay is a type of regularization method that reduces the weight by a small factor to avoid overfitting. Here, binary cross-entropy loss function is used for training binary classifiers. Other concepts of most important hyperparameters in networks are batch size and epochs. Larger batch size leads to faster training and develops a well-generalized model based on the unseen data. However, larger batch size depends on the computational power of the machine, that is, machine would be able to process the large batch of input data without crashing. The smaller batch size makes the learning slower but not less accurate. Therefore, the optimal batch size selected is 20 according to our machine and data (Figure 12.4).

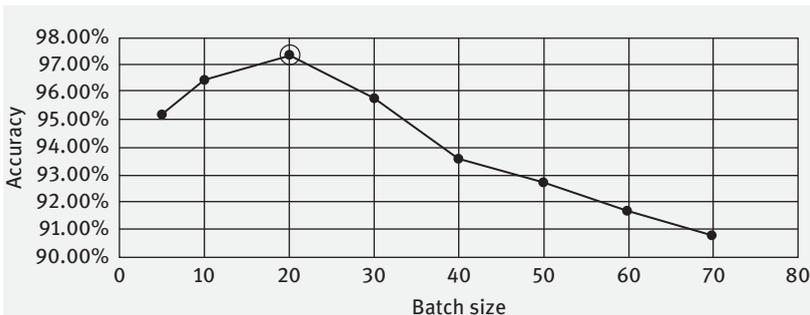


Figure 12.4: Maximum accuracy with a batch size of 20.

The sigmoid activation function performs the nonlinear transformation to the input, which makes it learn and perform more complex features efficiently.

Next, the experiment was conducted by varying the images in a dataset. It is observed that accuracy improves, and time taken for the training also rises as the number of images increases. With maximum available images in the dataset, the accuracy of 97.37% (Table 12.4) was obtained. However, a further increase in accuracy is not ruled out (Figure 12.5).

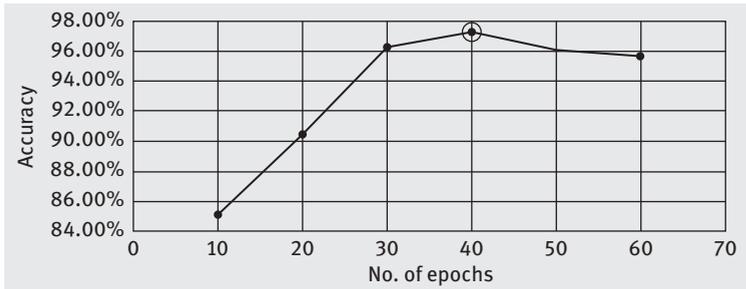


Figure 12.5: Maximum accuracy for epochs size of 40.

Table 12.4: Training time and accuracy varies with the number of images used for training.

No. of images	Time (s/epochs)	Accuracy (%)
100	186	76.0
200	275	77.5
500	394	83.3
1,000	498	90.2
1,500	761	93.6
2,000	1,524	97.37

12.7 Conclusion

DL method shows higher accuracy and uses images directly as input for automatic feature extraction in disease identification. CNN is identified as a suitable and powerful architecture for image-based disease identification. The proposed model achieves 97.37% accuracy, which is quite better than the performance of other models and techniques. The experimental result also reflects that to improve the accuracy, expanding the dataset would help in improving the generalization ability of the developed model. The results presented could be further extended to the development of a mobile application based on wheat disease identification.

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